PART III: ANTIBODY BINDING SITES

How to Use Part III:

Section 1: Anti-HIV Antibody Tables, Maps, and Index

This section summarizes HIV-specific antibodies arranged sequentially according to the location of their binding domain, organized by protein. We attempted to make this section as comprehensive as possible. For the MAbs capable of binding to linear peptides, we require that the binding site be contained within a region of 30 or so amino acids, but not that the precise boundaries be defined, for inclusion in the maps. MAbs that cannot bind to linear peptides are grouped by category at the end of each protein. For example, MAbs that inhibit sCD4 binding are grouped together at the end of the gp120 table. For more recent updates and search capabilities, please see our Web site: http://hiv-web.lanl.gov/immuno.

TABLES: Each MAb has an eight-part basic entry:

- **Number: Order of appearance in the database**
- **ID**
- **Location: The amino acid positions of the epitope boundaries and the reference sequence are listed as given in the primary publication.** Frequently, these positions as published are imprecise, and do not truly correspond to the numbering of the sequence, but they provide a reasonable guide to the peptide's approximate location in the protein. Also, in many cases the reference sequence identification was not provided. Binding sites that cannot be approximated through peptide binding or interference studies are labeled "dis" for "discontinuous". The approximate location on the protein, sequence number, and reference sequence are listed.
- **WEAU Location: Position of the binding site on the viral strain WEAU, used as a reference strain throughout this publication.** The position of the defined epitope's location on the sequence on the WEAU protein is indicated. The numbering corresponds to the protein maps. Epitopes that cannot be approximated through peptide binding or interference are labeled "dis" for discontinuous.
- **Sequence: The amino acid sequence of the binding region of interest as defined in the reference, based on the reference strain used in the study defining the binding site.** On rare occasions, when only the location and not the actual peptide sequence was specified in the original publication, and the sequences were numbered inaccurately by the primary authors, we may have misrepresented the binding site's amino acid sequence. Therefore, epitopes that were not explicitly written in the primary publication, that we determined by looking up the reference strain and the numbered location, are followed by a question mark in the table.
- **Neutralizing: L**: neutralizes lab strains. **P**: neutralizes primary isolates. **n**: does not neutralize.
- **Immunogen:** The antigenic stimulus of the B cell response.
- **Species(Isotype):**
- **References: All publications that we could find that refer to the use of a specific antibody.** First is a list of all references. Second is a list of the donors. This comes from the primary publications, and is meant to serve as a potential guide to a source of information about an antibody or how to obtain it, as well as to provide credit. Then comes a list of notes describing the context of the antibodies used in each study. MAb often have several names. For example punctuation can lost or names are often shortened (M-70 in one paper can be M70 in another). We attempt to include all of the Ab "nicknames" we encounter in the literature, so the search tools on the WEB site can find a given antibody.

MAPS:

The names of MAbs and the location of well characterized binding sites are indicated on protein sequences of the WEAU clone 1.60. This map is meant to provide the relative location of epitopes on a given protein, but the WEAU sequence may not actually bind to the MAb of interest, as it may vary relative to the sequence for which the epitope was defined. For more information concerning the WEAU sequence, see the CTL "How to use this section" guide in part I.

Two indices are provided. The first lists the MAbs IDs in alphabetical order so one can find their location in the database. The second provides a concise list of the MAbs in order of their appearance in the database, ordered by the protein coding regions spanning HIV-1.